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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2002, 18:42:27 ; Search time 179 seconds
(without alignments)
249.384 Million cell updates/sec

Title: US-09-794-764-195

Perfect score: 139
Sequence: 1 GKPNTNKSEAKRKSHTQTTOEICE 26

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Post-processing: Minimum Match 0%

Command line parameters: -DRV=xlh
-MODEL=frame+p2n.model -DRV=xlh
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-DB=N_Geneseq_032802 -QPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOP=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6 -FCGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_032802.*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
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- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
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- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	1460	19	Babesia microti BM
2	139	100.0	1460	19	Babesia microti an
3	139	100.0	1460	21	B. microti clone a
4	139	100.0	1820	19	Babesia microti BM
5	139	100.0	1820	19	Babesia microti BM
6	139	100.0	1820	20	Babesia microti an
7	139	100.0	1820	20	Babesia microti an
8	139	100.0	1820	21	B. microti BMNI-17
9	139	100.0	1820	21	B. microti BMNI-17
10	139	100.0	2001	21	B. microti MN-10/B
11	139	100.0	3402	21	B. microti MN-10/B
12	57	41.0	1760	23	Drosophila melanog
13	57	41.0	6725	23	Drosophila melanog
14	56	40.3	6200	22	Tumour suppressor
15	55.5	39.9	31449	23	Drosophila melanog
16	55	39.6	30889	23	Drosophila melanog
17	55	39.6	31563	23	Drosophila melanog
18	55	39.6	38189	23	Drosophila melanog
19	55	39.6	39814	23	Drosophila melanog
20	54	38.8	1866	22	Human colon cancer
21	54	38.8	43676	21	Nucleotide sequenc
22	53	38.1	473	21	Arabidopsis thalia
23	53	38.1	575	21	Arabidopsis thalia
24	53	38.1	5878	24	Human immune syste
25	52.5	37.8	801	21	Arabidopsis thalia
26	52	37.4	671	21	Arabidopsis thalia
27	51	36.7	3190	23	Drosophila melanog
28	51	36.7	5572	24	Human immune syste
29	51	36.7	6084	24	Human immune syste
30	51	36.7	8420	22	Tumour suppressor
31	51	36.7	12601	24	Human immune syste
32	51	36.7	35048	23	Drosophila melanog
33	51	36.7	45265	21	Sequence of a COSM
34	51	36.7	89024	23	Drosophila melanog
35	51	36.7	1230025	20	Nucleotide sequenc
36	51	36.0	704	21	Aspergillus oryzae
37	50	36.0	1455	22	C glutamicum codin
38	50	36.0	5511	24	Human immune syste
39	50	36.0	11116	22	Human polynucleoti
40	50	36.0	16033	24	Human immune syste
41	50	36.0	36635	23	Drosophila melanog
42	50	36.0	273254	21	Chlamydia pneumoni
43	50	36.0	349980	22	C glutamicum codin
44	49.5	35.6	1736	21	Morbillivirus anti
45	49.5	35.6	2331	23	DNA encoding novel

ALIGNMENTS

RESULT 1
AAV22749
ID AAV22749 standard; DNA; 1460 BP.

XX AAV22749;

XX 28-SEP-1998 (first entry)

XX Babesia microti BMNI-20 antigen sequence.

XX antigen; detection; diagnosis; vaccine; tick-borne disease;
XX differentiation; Lyme disease; ehrlichiosis; ss.

OS Babesia microti.

XX Key Location/Qualifiers

FT CDS 1..1509

FT /*tag= a

```

FT XX                                     /product= antigen
PN XX
XX EP834567-A2.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97EP-0117067.
XX
XX 24-APR-1997; 97US-0845258.
XX
XX 01-OCT-1996; 96US-0723142.
XX
XX (CORI-) CORIXA CORP.
XX
XX Houghton R, Lodes MJ, Reed SG, Sleath PR;
PI
XX WPI; 1998-195465/18.
XX
XX P-PSDB; AAW56303.
XX
XX Polypeptides comprising Babesia microti antigens and their
PT immunogenic fragments or epitopes - and related nucleic acid,
PT vectors, transformed cells and antibodies, useful for diagnosis of
PT infection and in protective vaccines
XX
XX Claim 8; Page 97-98; 113pp; English.
XX
XX The sequence is that encoding a polypeptide comprising at least
CC one antigenic portion of a Babesia microti antigen. It can be used
CC to diagnose B. microti infection by detecting specific antibodies
CC in usual immunoassays. Infection can also be diagnosed using:
CC (a) primers or probes derived from the coding sequence, in
CC standard amplification or hybridisation tests, or (b) using
CC antibodies to detect the corresponding antigen. It is also
CC useful in vaccines to protect against infection, especially
CC when formulated with an adjuvant. The new diagnostic methods
CC allow rapid differentiation between B. microti infection and
CC other tick-borne diseases (Lyme disease and ehrlichiosis) that
CC have similar symptoms but require different treatments.
XX
XX SQ Sequence 1460 BP; 539 A; 252 C; 283 G; 386 T; 0 other;

Alignment Scores:
Pred. No.: 2.97e-13 Length: 1460
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-794-764-195 (1-26) x AAV22749 (1-1460)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1287 GGCAACCCCAATACGATAAAAGTGAGAAGGCTGAAGAAAATCGCATGATCTACGACA 1346
Qy 21 ThrGlnGluLeuCysGlu 26
Db 1347 ACGCAAGAAATATGTGAA 1364

RESULT 2
AAC90017
ID AAC90017 standard; DNA; 1460 BP.
XX
XX AAC90017;
XX
XX 16-SEP-1999 (first entry)
XX
XX Babesia microti antigen BMNI-20 complementary open reading frame.
XX
XX Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
KW immunity; detection; ss.
XX
XX Babesia microti.
OS
XX

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PN W09929869-A1.
XX
XX 17-JUN-1999.
XX
XX 11-DEC-1998; 98WO-US26437.
XX
XX 11-DEC-1997; 97US-0990571.
XX
XX (CORI-) CORIXA CORP.
XX
XX (MAYO-) MAYO FOUNDATION.
XX
XX Bruinsma E, Houghton R, Lodes MJ, Persing D, Reed SG;
PI Sleath PR;
XX
XX WPI; 1999-385612/32.
XX
XX P-PSDB; AAY24365.
XX
XX New isolated Babesia microti polypeptides
PT
XX Example 1; Page 106-107; 126pp; English.
XX
XX The present invention describes isolated polypeptides comprising
CC specific immunogenic portions of Babesia microti. AAX88983 to AAX88994
CC encode specifically claimed B. microti immunogenic proteins, and
CC AAY24327 to AAY24338 represent these proteins. B. microti polypeptides
CC and nucleic acids can be used for detecting B. microti infections. They
CC can also be used in vaccines for inducing protective immunity against B.
CC microti infections. The present sequence encodes a B. microti antigen.
XX
XX SQ Sequence 1460 BP; 539 A; 252 C; 283 G; 386 T; 0 other;

Alignment Scores:
Pred. No.: 2.97e-13 Length: 1460
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-794-764-195 (1-26) x AAX90017 (1-1460)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1287 GGCAACCCCAATACGATAAAAGTGAGAAGGCTGAAGAAAATCGCATGATCTACGACA 1346
Qy 21 ThrGlnGluLeuCysGlu 26
Db 1347 ACGCAAGAAATATGTGAA 1364

RESULT 3
AAC65100
ID AAC65100 standard; DNA; 1460 BP.
XX
XX AAC65100;
XX
XX 12-FEB-2001 (first entry)
XX
XX B. microti clone antigen coding sequence SEQ ID NO: 51.
XX
XX Babesiosis; rodent parasite; tick-borne illness; antigen;
KW disease diagnosis; disease prevention; ds.
XX
XX Babesia microti.
OS
XX
XX W0200060090-A1.
PN
XX 12-OCT-2000.
XX
XX 05-APR-2000; 2000WO-US09136.
XX
XX 05-APR-1999; 99US-0286488.
XX
XX 17-MAR-2000; 2000US-0528784.
XX

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PA (CORI-) CORIXA CORP.
XX Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;
XX WPI; 2000-686939/67.
XX New polypeptides containing an antigenic portion of Babesia microti
PT antigen and DNAs encoding the polypeptides, useful for diagnosing,
PT treating or preventing B. microti infection, or for inducing protective
PT immunity in a patient
XX Claim 1; Page 96; 118pp; English.
XX The present invention is related to the isolation of antigenic sequences
CC from the rodent parasite Babesia microti. This organism is transmitted to
CC humans by the same tick which transmits Lyme disease and ehrlichiosis.
CC The organism causes a malaria-like infection known as babesiosis. The
CC sequences identified by this invention can be used in the diagnosis,
CC prevention and treatment of babesiosis.
XX Sequence 1460 BP; 539 A; 252 C; 283 G; 386 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 2.97e-13 Length: 1460
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-794-764-195 (1-26) x AAC65100 (1-1460)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1287 GGCAAAACCCCAATACGAATAAAGTGAGAAGGCTGAAAGAAATCGCATGATCTACTCAGACA 1346
Qy 21 ThrGlnGluLeuCysGlu 26
Db 1347 ACGCAAGAAATATGTGAA 1364
RESULT 4
AAV22747/c
ID AAV22747 standard; DNA; 1820 BP.
XX AAV22747;
AC AAV22747;
DT 28-SEP-1998 (first entry)
XX Babesia microti BMNI-17 antigen sequence.
XX antigen; detection; diagnosis; vaccine; tick-borne disease;
KW differentiation; Lyme disease; ehrlichiosis; ss.
XX Babesia microti.
XX Key Location/Qualifiers
FH 98..832
FT /*tag= a
FT /product= antigen
XX EP834567-A2.
XX 08-APR-1998.
XX 01-OCT-1997; 97EP-0117067.
XX 24-APR-1997; 97US-0845258.
XX 01-OCT-1996; 96US-0723142.
XX (CORI-) CORIXA CORP.
PA Houghton R, Lodes MJ, Reed SG, Sleath PR;
XX

DR WPI; 1998-195465/18.
DR P-PSDB; AAW56297.
XX Polypeptides comprising Babesia microti antigens and their
PT immunogenic fragments or epitopes - and related nucleic acid,
PT vectors, transformed cells and antibodies, useful for diagnosis of
PT infection and in protective vaccines
XX Claim 8; Page 43-44; 113pp; English.
XX The sequence is that encoding a polypeptide comprising at least
CC one antigenic portion of a Babesia microti antigen. It can be used
CC to diagnose B. microti infection by detecting specific antibodies
CC in usual immunoassays. Infection can also be diagnosed using:
CC (a) primers or probes derived from the coding sequence, in
CC standard amplification or hybridisation tests, or (b) using
CC antibodies to detect the corresponding antigen. It is also
CC useful in vaccines to protect against infection, especially
CC when formulated with an adjuvant. The new diagnostic methods
CC allow rapid differentiation between B. microti infection and
CC other tick-borne diseases (Lyme disease and ehrlichiosis) that
CC have similar symptoms but require different treatments.
XX Sequence 1820 BP; 402 A; 398 C; 334 G; 686 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 3.89e-13 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0
US-09-794-764-195 (1-26) x AAV22747 (1-1820)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 793 GGCAAAACCCCAATACGAATAAAGTGAGAAGGCTGAAAGAAATCGCATGATCTACTCAGACA 734
Qy 21 ThrGlnGluLeuCysGlu 26
Db 733 ACGCAAGAAATATGTGAA 716
RESULT 5
AAV22753
ID AAV22753 standard; DNA; 1820 BP.
XX AAV22753;
AC AAV22753;
DT 28-SEP-1998 (first entry)
XX Babesia microti BMNI-17 antigen complement sequence.
XX antigen; detection; diagnosis; vaccine; tick-borne disease;
KW differentiation; Lyme disease; ehrlichiosis; ss.
XX Babesia microti.
XX Key Location/Qualifiers
FH complement (98..832)
FT /*tag= a
FT /product= antigen
XX EP834567-A2.
XX 08-APR-1998.
XX 01-OCT-1997; 97EP-0117067.
XX 24-APR-1997; 97US-0845258.
XX 01-OCT-1996; 96US-0723142.
XX (CORI-) CORIXA CORP.
PA

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XX Houghton R, Lodes MJ, Reed SG, Sleath PR;
PI WPI; 1998-195465/18.
XX P-PSDB; AAW56298.
XX Polypeptides comprising Babesia microti antigens and their
PT immunogenic fragments or epitopes - and related nucleic acid,
PT vectors, transformed cells and antibodies, useful for diagnosis of
PT infection and in protective vaccines
XX Claim 8; Page 75-77; 113pp; English.
XX The sequence is that encoding a polypeptide comprising at least
CC one antigenic portion of a Babesia microti antigen. It can be used
CC to diagnose B. microti infection by detecting specific antibodies
CC in usual immunoassays. Infection can also be diagnosed using:
CC (a) primers or probes derived from the coding sequence, in
CC standard amplification or hybridisation tests, or (b) using
CC antibodies to detect the corresponding antigen. It is also
CC useful in vaccines to protect against infection, especially
CC when formulated with an adjuvant. The new diagnostic methods
CC allow rapid differentiation between B. microti infection and
CC other tick-borne diseases (Lyme disease and ehrlichiosis) that
CC have similar symptoms but require different treatments.
XX
SQ Sequence 1820 BP; 686 A; 334 C; 398 G; 402 T; 0 other;

Alignment Scores:
Pred. No.: 3.89e-13 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-794-764-195 (1-26) x AAV22753 (1-1820)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1028 GGCAAAACCCAAATACGAAATAAAGTGAGAGGCTGAAGAAATCGCATGACTCAGACA 1087

Qy 21 ThrGlnGluLeuCysGlu 26
Db 1088 ACGCAAGAAATATGTGAA 1105

RESULT 6
AAX90011/C
ID AAX90011 standard; DNA; 1820 BP.
XX AAX90011;
XX 16-SEP-1999 (first entry)
XX Babesia microti antigen BMNI-17 encoding DNA.
XX Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
KW immunity; detection; ss.
XX Babesia microti.
OS WO9929869-A1.
XX 17-JUN-1999.
XX 11-DEC-1998; 98WO-US26437.
XX 11-DEC-1997; 97US-0990571.
XX (CORI-) CORIXA CORP.
PA (MAYO-) MAYO FOUNDATION.
XX Bruinsma E, Houghton R, Lodes MJ, Persing D, Reed SG;
PI Sleath PR;
XX WPI; 1999-385612/32.
XX P-PSDB; AAY24358.
XX New isolated Babesia microti polypeptides
Example 1; Page 90-91; 126pp; English.

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PI Sleath PR;
XX WPI; 1999-385612/32.
XX P-PSDB; AAY24353.
XX New isolated Babesia microti polypeptides
Example 1; Page 67-68; 126pp; English.
XX The present invention describes isolated polypeptides comprising
CC specific immunogenic portions of Babesia microti. AAX88983 to AAX88994
CC encode specifically claimed B. microti immunogenic proteins, and
CC AAY24327 to AAY24338 represent these proteins. B. microti polypeptides
CC and nucleic acids can be used for detecting B. microti infections. They
CC can also be used in vaccines for inducing protective immunity against B.
CC microti infections. The present sequence encodes a B. microti antigen.
XX
SQ Sequence 1820 BP; 402 A; 398 C; 334 G; 686 T; 0 other;

Alignment Scores:
Pred. No.: 3.89e-13 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-794-764-195 (1-26) x AAX90011 (1-1820)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 793 GGCAAAACCCAAATACGAAATAAAGTGAGAGGCTGAAGAAATCGCATGACTCAGACA 734

Qy 21 ThrGlnGluLeuCysGlu 26
Db 733 ACGCAAGAAATATGTGAA 716

RESULT 7
AAX90012
ID AAX90012 standard; DNA; 1820 BP.
XX AAX90012;
XX 16-SEP-1999 (first entry)
XX Babesia microti antigen BMNI-17 complementary open reading frame.
XX Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
KW immunity; detection; ss.
XX Babesia microti.
OS WO9929869-A1.
XX 17-JUN-1999.
XX 11-DEC-1998; 98WO-US26437.
XX 11-DEC-1997; 97US-0990571.
XX (CORI-) CORIXA CORP.
PA (MAYO-) MAYO FOUNDATION.
XX Bruinsma E, Houghton R, Lodes MJ, Persing D, Reed SG;
PI Sleath PR;
XX WPI; 1999-385612/32.
XX P-PSDB; AAY24358.
XX New isolated Babesia microti polypeptides
Example 1; Page 90-91; 126pp; English.

```

CC The present invention describes isolated polypeptides comprising
CC specific immunogenic portions of Babesia microti. AAX88983 to AAX88994
CC encode specifically claimed B. microti immunogenic proteins, and
CC AAY24327 to AAY24338 represent these proteins. B. microti polypeptides
CC and nucleic acids can be used for detecting B. microti infections. They
CC can also be used in vaccines for inducing protective immunity against B.
CC microti infections. The present sequence encodes a B. microti antigen.
XX
SQ Sequence 1820 BP; 686 A; 334 C; 398 G; 402 T; 0 other;

Alignment Scores:
Pred. No.: 3.89e-13 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-794-764-195 (1-26) x AAX90012 (1-1820)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
|||||
DB 1028 GGCAACCCCAATACGAATAAAGTGAGAGGCTGAAGAAATCGCATGATCTACTCAGACA 1087

QY 21 ThrGlnGluLeuCysGlu 26
|||||
DB 1088 ACGCAAGAAATATGTGAA 1105

RESULT 8

AAC65094/c
ID AAC65094 standard; DNA; 1820 BP.

XX AAC65094;

XX 12-FEB-2001 (first entry)

DE B. microti BMNI-17 antigen coding sequence SEQ ID NO: 17.
XX
XX Babesiosis; rodent parasite; tick-borne illness; antigen;
KW disease diagnosis; disease prevention; ds.
XX

OS Babesia microti.

XX WO200060090-A1.

XX 12-OCT-2000.

XX 05-APR-2000; 2000WO-US09136.

XX 05-APR-1999; 99US-0286488.

XX 17-MAR-2000; 2000US-0528784.

XX (CORI-) CORIXA CORP.

XX Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;

XX WPI; 2000-686939/67.

XX P-PSDB; AAB30202.

XX New polypeptides containing an antigenic portion of Babesia microti
PT antigen and DNAs encoding the polypeptides, useful for diagnosing,
PT treating or preventing B. microti infection, or for inducing protective
PT immunity in a patient

XX Claim 1; Page 69; 118pp; English.

XX The present invention is related to the isolation of antigenic sequences
CC from the rodent parasite Babesia microti. This organism is transmitted to
CC humans by the same tick which transmits Lyme disease and ehrlichiosis.
CC The organism causes a malaria-like infection known as babesiosis. The
CC sequences identified by this invention can be used in the diagnosis,
CC prevention and treatment of babesiosis.

SQ Sequence 1820 BP; 402 A; 398 C; 334 G; 686 T; 0 other;
Alignment Scores:
Pred. No.: 3.89e-13 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-794-764-195 (1-26) x AAC65094 (1-1820)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
|||||
DB 793 GGCAACCCCAATACGAATAAAGTGAGAGGCTGAAGAAATCGCATGATCTACTCAGACA 734

QY 21 ThrGlnGluLeuCysGlu 26
|||||
DB 733 ACGCAAGAAATATGTGAA 716

RESULT 9

AAC65095
ID AAC65095 standard; DNA; 1820 BP.

XX AAC65095;

XX 12-FEB-2001 (first entry)

DE B. microti BMNI-17 antigen reverse complement SEQ ID NO: 37.

XX Babesiosis; rodent parasite; tick-borne illness; antigen;
KW disease diagnosis; disease prevention; ds.
XX

OS Babesia microti.

XX WO200060090-A1.

XX 12-OCT-2000.

XX 05-APR-2000; 2000WO-US09136.

XX 05-APR-1999; 99US-0286488.

XX 17-MAR-2000; 2000US-0528784.

XX (CORI-) CORIXA CORP.

XX Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;

XX WPI; 2000-686939/67.

XX New polypeptides containing an antigenic portion of Babesia microti
PT antigen and DNAs encoding the polypeptides, useful for diagnosing,
PT treating or preventing B. microti infection, or for inducing protective
PT immunity in a patient

XX Example 1; Page 86; 118pp; English.

XX The present invention is related to the isolation of antigenic sequences
CC from the rodent parasite Babesia microti. This organism is transmitted to
CC humans by the same tick which transmits Lyme disease and ehrlichiosis.
CC The organism causes a malaria-like infection known as babesiosis. The
CC sequences identified by this invention can be used in the diagnosis,
CC prevention and treatment of babesiosis.

XX Sequence 1820 BP; 686 A; 334 C; 398 G; 402 T; 0 other;

Alignment Scores:
Pred. No.: 3.89e-13 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-794-764-195 (1-26) x AAC65095 (1-1820)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
 Db 1028 GGCAAAACCCATACGATATAAAAGTGAGAGGCTGAAGAAATCGCATGATCTACAGACA 1087

Qy 21 ThrGlnGluLeuCysGlu 26
 Db 1088 ACACAAGAAATATGTGAA 1105

RESULT 10
 AAC65119
 ID AAC65119 standard; cDNA; 2001 BP.
 XX
 AC AAC65119;
 XX
 DT 12-FEB-2001 (first entry)
 XX
 DE B. microti MN-10/BMNI-17 fusion protein cDNA SEQ ID NO: 84.
 XX
 KW Babesiosis; rodent parasite; tick-borne illness; antigen;
 KW disease diagnosis; disease prevention; ss.
 XX
 OS Babesia sp.
 XX
 PN WO200060090-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 05-APR-2000; 2000WO-US09136.
 XX
 PR 05-APR-1999; 99US-0286488.
 PR 17-MAR-2000; 2000US-0528784.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;
 DR WPI; 2000-686939/67.
 XX
 PT New polypeptides containing an antigenic portion of Babesia microti
 PT antigen and DNAs encoding the polypeptides, useful for diagnosing,
 PT treating or preventing B. microti infection, or for inducing protective
 PT immunity in a patient
 XX
 PS Example 5; Page 108; 118pp; English.
 XX
 CC The present invention is related to the isolation of antigenic sequences
 CC from the rodent parasite Babesia microti. This organism is transmitted to
 CC humans by the same tick which transmits Lyme disease and ehrlichiosis.
 CC The organism causes a malaria-like infection known as babesiosis. The
 CC sequences identified by this invention can be used in the diagnosis,
 CC prevention and treatment of babesiosis.
 XX
 SQ Sequence 2001 BP; 742 A; 334 C; 462 G; 463 T; 0 other;

Alignment Scores:
 Pred. No.: 4.37e-13 Length: 2001
 Score: 139.00 Matches: 26
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-794-764-195 (1-26) x AAC65119 (1-2001)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
 Db 1207 GGCAAAACCCATACGATATAAAAGTGAGAGGCTGAAGAAATCGCATGATCTACAGACA 1266

Qy 21 ThrGlnGluLeuCysGlu 26
 Db 1088 ACACAAGAAATATGTGAA 1105

RESULT 11
 AAC65120
 ID AAC65120 standard; cDNA; 3402 BP.
 XX
 AC AAC65120;
 XX
 DT 12-FEB-2001 (first entry)
 XX
 DE B. microti MN-10/BMNI-17/BMNI-15 fusion protein cDNA SEQ ID NO: 86.
 XX
 KW Babesiosis; rodent parasite; tick-borne illness; antigen;
 KW disease diagnosis; disease prevention; ss.
 XX
 OS Babesia sp.
 XX
 PN WO200060090-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 05-APR-2000; 2000WO-US09136.
 XX
 PR 05-APR-1999; 99US-0286488.
 PR 17-MAR-2000; 2000US-0528784.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;
 DR WPI; 2000-686939/67.
 XX
 PT New polypeptides containing an antigenic portion of Babesia microti
 PT antigen and DNAs encoding the polypeptides, useful for diagnosing,
 PT treating or preventing B. microti infection, or for inducing protective
 PT immunity in a patient
 XX
 PS Example 5; Page 111-112; 118pp; English.
 XX
 CC The present invention is related to the isolation of antigenic sequences
 CC from the rodent parasite Babesia microti. This organism is transmitted to
 CC humans by the same tick which transmits Lyme disease and ehrlichiosis.
 CC The organism causes a malaria-like infection known as babesiosis. The
 CC sequences identified by this invention can be used in the diagnosis,
 CC prevention and treatment of babesiosis.
 XX
 SQ Sequence 3402 BP; 1184 A; 615 C; 712 G; 891 T; 0 other;

Alignment Scores:
 Pred. No.: 8.41e-13 Length: 3402
 Score: 139.00 Matches: 26
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-794-764-195 (1-26) x AAC65120 (1-3402)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
 Db 2605 GGCAAAACCCATACGATATAAAAGTGAGAGGCTGAAGAAATCGCATGATCTACAGACA 2664

Qy 21 ThrGlnGluLeuCysGlu 26
 Db 2665 ACACAAGAAATATGTGAA 2682

RESULT 12
 ABL15763
 ID ABL15763 standard; cDNA; 1760 BP.
 XX
 AC ABL15763;
 XX
 DT 26-MAR-2002 (first entry)


```

KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX P-PSDB; ABB71659.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 41768; 2lpp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 6725 BP; 2026 A; 1267 C; 1347 G; 2085 T; 0 other;

Alignment Scores:
Pred. No.: 61.8 Length: 6725
Score: 57.00 Matches: 12
Percent Similarity: 58.33% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 10
Query Match: 41.01% Indels: 0
DB: 23 Gaps: 0

US-09-794-764-195 (1-26) x ABL15762 (1-6725)
QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluAluGlySerHisAspThrGlnThr 20
Db 5439 GCCGTCACATACAAAAGCCGAAAGGAATCAATTACAGTAGTGCTCAACAACGC 5380
QY 21 ThrGlnGluIle 24
Db 5379 GCCCAGGAAGTC 5368

RESULT 14
AAS46442/C
ID AAS46442 standard; DNA; 6200 BP.
XX
XX AAS46442;
XX
XX 18-DEC-2001 (first entry)
XX
XX Tumour suppressor gene derived chemically modified sequence #164.
XX
XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
XX cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
XX cytosine methylation; ds.
XX
XX Homo sapiens.

```

```
XX PN WO200168912-A2.
XX PD 20-SEP-2001.
XX PF 15-MAR-2001; 2001WO-EP02955.
XX PR 15-MAR-2000; 2000DE-1013847.
XX PR 06-APR-2000; 2000DE-1019058.
XX PR 07-APR-2000; 2000DE-1019173.
XX PR 30-JUN-2000; 2000DE-1032529.
XX PR 01-SEP-2000; 2000DE-1043826.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-602752/68.
XX PT Fragments of chemically modified genes associated with tumour suppressor
XX PT genes and oncogenes, useful in designing primers and probes for
XX PT analysing diseases associated with cytosine methylation state e.g.
XX PT cancer
XX PS Claim 1; SEQ ID No 164; 27pp; English.
XX CC The invention relates to a nucleic acid comprising a sequence of 18
XX CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
XX CC bisulphite, of genes associated with tumour suppression and
XX CC oncogenes having a sequence taken from 536 (actually 533 since
XX CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
XX CC (SS) and sequences complementary to (SS). The nucleic acid may be a
XX CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
XX CC form part of a set of probes for detecting the cytosine methylation state
XX CC and/or single nucleotide polymorphisms and also to be used in an
XX CC array for analysing diseases associated with CpG dinucleotides e.g.
XX CC cancers and tumours. The probes can also be used in a method for
XX CC ascertaining genetic and/or epigenetic parameters for the diagnosis
XX CC and/or therapy of existing diseases or the predisposition to specific
XX CC diseases, by analysing cytosine methylations. The parameters may be
XX CC compared to another set of genetic and/or epigenetic parameters, the
XX CC differences serving as basis for diagnosis and/or prognosis events which
XX CC are disadvantageous to patients. The present sequence is one of the
XX CC 533 genomic sequences derived from tumour suppressor genes and
XX CC oncogenes. Sequences with even numbered Seq ID numbers are the
XX CC complementary sequences of the corresponding odd numbered sequence (e.g.
XX CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
XX CC is missing).
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SO Sequence 6200 BP; 1487 A; 134 C; 1522 G; 3057 T; 0 other;

Alignment Scores:
Pred. No.: 81.7 Length: 6200
Score: 56.00 Matches: 11
Percent Similarity: 60.00% Conservative: 1
Best Local Similarity: 55.00% Mismatches: 8
Query Match: 40.29% Indels: 0
DB: 22 Gaps: 0

US-09-794-764-195 (1-26) x AAS46442 (1-6200)
Qy 3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrGln 22
Db 1231 CCGCAAAAAACCAAAAAACGAAACGACGACTCTCGCCACGACACCAAACTACGGC 1172
RESULT 15
ABL09172/C
ID ABL09172 standard; cDNA: 31449 BP.
XX
```

```
AC ABL09172;
XX 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21998.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS pharmaceutical; gene; ss.
XX PN Drosophila melanogaster.
XX PD WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR P-PSDB; ABB65069.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PS interactions -
XX PS Claim 1; SEQ ID NO 21998; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins
XX CC (ABB57737-ABB72072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 31449 BP; 9180 A; 6598 C; 6566 G; 9105 T; 0 other;

Alignment Scores:
Pred. No.: 729 Length: 31449
Score: 55.50 Matches: 12
Percent Similarity: 65.22% Conservative: 3
Best Local Similarity: 52.17% Mismatches: 7
Query Match: 39.93% Indels: 1
DB: 23 Gaps: 1

US-09-794-764-195 (1-26) x ABL09172 (1-31449)
Qy 3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrGln 22
Db 29046 CCGAAACCAACATAAAGTAAACAAAAACAAACAAAGTACACAC---ACGCTCAGCACACA 28990
Qy 23 GluileCys 25
Db 28989 GAGATATGC 28981

Search completed: October 12, 2002, 20:55:49
Job time : 183 secs
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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2002, 18:42:28 ; Search time 1833 Seconds
(without alignments)
296.830 Million cell updates/sec

Title: US-09-794-764-195
Perfect score: 139
Sequence: 1 GKPNTNKSEAKERSHDTQTQICE 26

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Listing first 45 summaries

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13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*

29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	139	100.0	1460	3	AF206527	Babesia m
2	139	100.0	1460	6	ARI29329	Sequence
3	139	100.0	1460	6	AX304537	Sequence
4	139	100.0	1820	3	AF206526	Babesia m
5	139	100.0	1820	6	ARI29323	Sequence
6	139	100.0	1820	6	ARI29324	Sequence
7	139	100.0	1820	6	ARI73458	Sequence
8	139	100.0	1820	6	ARI73459	Sequence
9	139	100.0	1820	6	AX304503	Sequence
10	139	100.0	1820	6	AX304523	Sequence
11	139	100.0	2001	6	AX304570	Sequence
12	139	100.0	2034	6	AX304629	Sequence
13	139	100.0	2079	6	AX304696	Sequence
14	139	100.0	3402	6	AX304572	Sequence
15	68	48.9	20094	2	AC020862	Mus muscu
16	61	43.9	212637	2	AL662919	Mus muscu
17	61	43.9	223926	2	AL645993	Mus muscu
18	60.5	43.5	26497	3	CEFA0F8	Caenorhabdi
19	60	43.2	59029	9	AL445163	Human DNA
20	60	43.2	144333	2	AC097962	Rattus no
21	59	42.4	63671	2	AC100417	Mus muscu
22	58.5	42.1	112484	2	AC103259	Rattus no
23	58	41.7	141271	2	CNS01DUL	Homo sapi
24	58	41.7	167979	2	AL354770	Homo sapi
25	57	41.0	920	33	AC029651	Giardia i
26	57	41.0	2237	3	AY061256	Drosophila
27	57	41.0	2243	3	DMU30603	Drosophila
28	57	41.0	6405	14	AF020051	Blackcurr
29	57	41.0	16706	2	AC015093	Drosophila
30	57	41.0	105000	9	AP002988	Homo sapi
31	57	41.0	113606	8	AC087192	Oryza sat
32	57	41.0	133936	9	HSDJ383J4	Human DNA
33	57	41.0	171493	2	AC021438	Homo sapi
34	57	41.0	179396	3	AC022351	Drosophila
35	57	41.0	223734	2	AC073750	Mus muscu
36	57	41.0	239254	2	AC079569	Mus muscu
37	57	41.0	301980	3	AE003502	Drosophila
38	56.5	40.6	154966	2	AF001387	Homo sapi
39	56.5	40.6	155847	9	AC090415	Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
Babesia microti strain MN1 seroreactive antigen BBN1-20 gene, partial cds.
ACCESSION
AF206527
VERSION
AF206527.1
KEYWORDS
Babesia microti.
SOURCE

AF206527
Babesia microti strain MN1 seroreactive antigen BBN1-20 gene, partial cds.
AF206527
AF206527.1
GI:7716018

1460 bp
DNA
linear
INV 08-MAY-2000

ORGANISM Babesia microti
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
REFERENCE 1 (bases 1 to 1460)
AUTHORS Lodes M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R.,
Reynolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H.
TITLE Serological expression cloning of novel immunoreactive antigens of
Babesia microti
JOURNAL Infect. Immun. 68 (5), 2783-2790 (2000).
MEDLINE 20231818
PUBMED 10768973
REFERENCE 2 (bases 1 to 1460)
AUTHORS Lodes, M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R.,
Reynolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-1999) Corixa Corporation, 1124 Columbia Street,
Suite 200, Seattle, WA 98104, USA
FEATURES
source 1..1460
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/strain="MN1"
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BASE COUNT 539 a 252 c 283 g 386 t
ORIGIN
Alignment Scores:
Pred. No.: 5,55e-12 Length: 1460
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-794-764-195 (1-26) x AF206527 (1-1460)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1287 GGCAAAACCAATACCAATAAAGTGAAGGCTGAAGAAATCGCATGATCTAGACA 1346
Qy 21 ThrGlnGluIleCysGlu 26
Db 1347 ACGCAAGAAATATGTGAA 1364
RESULT 2
AR129329 1460 bp DNA linear PAT 16-MAY-2001
LOCUS AR129329
DEFINITION Sequence 51 from patent US 6183976.
ACCESSION AR129329
VERSION AR129329.1 GI:14116991
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1460)
AUTHORS Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.
TITLE Compounds and methods for the diagnosis and treatment of B. microti
infection
JOURNAL Patent: US 6183976-A 51 06-FEB-2001;
FEATURES Location/Qualifiers

source 1..1460
/organism="unknown"
BASE COUNT 539 a 252 c 283 g 386 t
ORIGIN
Alignment Scores:
Pred. No.: 5,55e-12 Length: 1460
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-794-764-195 (1-26) x AR129329 (1-1460)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1287 GGCAAAACCAATACCAATAAAGTGAAGGCTGAAGAAATCGCATGATCTAGACA 1346
Qy 21 ThrGlnGluIleCysGlu 26
Db 1347 ACGCAAGAAATATGTGAA 1364
RESULT 3
AX304537 1460 bp DNA linear PAT 30-NOV-2001
LOCUS AX304537
DEFINITION Sequence 51 from Patent WO0185947.
ACCESSION AX304537
VERSION AX304537.1 GI:17383870
KEYWORDS Babesia microti.
SOURCE Babesia microti.
ORGANISM Babesia microti.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
REFERENCE 1 (sites)
AUTHORS Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., McNeill, P.D.,
Homer, M.J. and Secrist, H.
TITLE Compounds and methods for the diagnosis and treatment of Babesia
microti infection
JOURNAL Patent: WO 0185947-A 51 15-NOV-2001;
FEATURES CORIXA CORPORATION (US)
source 1..1460
/organism="Babesia microti"
/db_xref="taxon:5868"
BASE COUNT 539 a 252 c 283 g 386 t
ORIGIN
Alignment Scores:
Pred. No.: 5,55e-12 Length: 1460
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-794-764-195 (1-26) x AX304537 (1-1460)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1287 GGCAAAACCAATACCAATAAAGTGAAGGCTGAAGAAATCGCATGATCTAGACA 1346
Qy 21 ThrGlnGluIleCysGlu 26
Db 1347 ACGCAAGAAATATGTGAA 1364
RESULT 4
AF206526 1820 bp DNA linear INV 08-MAY-2000
LOCUS AF206526
DEFINITION Babesia microti strain MN1 seroreactive antigen BMN1-17 gene,
partial cds; and seroreactive antigen BMN1-17B gene, complete cds.
ACCESSION AF206526
VERSION AF206526.1 GI:7716015

KEYWORDS Babesia microti.
SOURCE Babesia microti.
ORGANISM Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.

REFERENCE 1 (bases 1 to 1820)
AUTHORS Lodes, M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R.,
Reynolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H.
TITLE Serological expression cloning of novel immunoreactive antigens of
Babesia microti.
JOURNAL Infect. Immun. 68 (5), 2783-2790 (2000)
MEDLINE 20231818
PUBMED 10768973

REFERENCE 2 (bases 1 to 1820)
AUTHORS Lodes, M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R.,
Reynolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-1999) Corixa Corporation, 1124 Columbia Street,
Suite 200, Seattle, WA 98104, USA
FEATURES
source
1..1820
/organism="Babesia microti"
/strain="MNI"
/db_xref="taxon:5868"
632..>1820
/function="unknown"
/notes="putative transmembrane protein"
/codon_start=1
/product="seroreactive antigen BMNL-17"
/protein_id="AAF68253.1"
/db_xref="GI:7716016"
/translation="MDSDTRVLPESLDEGVPHQFSLRGLHSDMASDINDEPSPFKIGE
NDLIQPPWEDTAPYHSIDDELDNLMRLTAQETSDOHEEGNGLNTKSEKTKRSHD
TQTPQIYELDNLRLTAQEIYEEKRGKGNKSEKAEKSHDTQTQICBEC
EEGHKINKNSGNAGIKSYDTQTQICECEEGHDKINKNSGNAGIKSYDTQTPQ
ETSDAHEEGHDKNTNKSEKAEKSHDTQTQICECEEGHDKINKNSGNAGIKSY
DTQTPQETSDAHEEGHDKINKNSGNAGIKSHNTQTPKKKFCCKEKGCHGNKPN
ERQSPDDGGGCEGNTNHFVDYKTKLLKSLKTSHTYIYIAAAITSLFPCP
FKAF"
complement(936..1606)
/function="unknown"
/note="putative type IIb membrane protein"
/codon_start=1
/product="seroreactive antigen BMNL-17B"
/protein_id="AAF68254.1"
/db_xref="GI:7716017"
/translation="MTPTFKVFFQRCLSIMRFYSSLPFLIETAMLFMSVTCFL
RCLSIIRFYSSITFLIDFVMPFFTLFTYFLRCLSIMRFSLLTIRIDFVMPFM
SVTCFLRCLSIIRFYSSITFLIDFVMPFFTLFTYFLRCLSIIRFYSSITFLIDF
VMPFFTLFTYFLRCLSIIMRFSLLTIRIGFAMPFTLIYFLCR"
repeat_region 989..1568
/note="encodes six 32 amino acid repeats"
/rpt_type=tandem
1757..1816
/note="transmembrane-region site"

BASE COUNT 686 a 334 c 398 g 402 t
ORIGIN

Alignment Scores:
Pred. No.: 7e-12 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-794-764-195 (1-26) x AF206536 (1-1820)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1028 GGCAAAACCAATACGAATAAAGTGAGAGGCTGAGAAATCGCATGACTACGACA 1087
Qy 21 ThrGlnGluLeuCysGlu 26

Db 1088 ACGAAGAATAATGTGAA 1105

RESULT 5
LOCUS ARL29323/c
DEFINITION Sequence 17 from patent US 6183976.
ACCESSION ARL29323
VERSION ARL29323.1 GI:14116985
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1820)
AUTHORS Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.
TITLE Compounds and methods for the diagnosis and treatment of B. microti
infection
JOURNAL Patent: US 6183976-A 17 06-FEB-2001;
FEATURES
Location/Qualifiers
1..1820
/organism="unknown"
BASE COUNT 402 a 398 c 334 g 686 t
ORIGIN

Alignment Scores:
Pred. No.: 7e-12 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-794-764-195 (1-26) x ARL29323 (1-1820)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 793 GGCAAAACCAATACGAATAAAGTGAGAGGCTGAGAAATCGCATGACTACGACA 734
Qy 21 ThrGlnGluLeuCysGlu 26

Db 733 ACGAAGAATAATGTGAA 716

RESULT 6
LOCUS ARL29324
DEFINITION Sequence 37 from patent US 6183976.
ACCESSION ARL29324
VERSION ARL29324.1 GI:14116986
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1820)
AUTHORS Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.
TITLE Compounds and methods for the diagnosis and treatment of B. microti
infection
JOURNAL Patent: US 6183976-A 37 06-FEB-2001;
FEATURES
Location/Qualifiers
1..1820
/organism="unknown"
BASE COUNT 686 a 334 c 398 g 402 t
ORIGIN

Alignment Scores:
Pred. No.: 7e-12 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-794-764-195 (1-26) x ARL29324 (1-1820)

Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-794-764-195 (1-26) x AR173459 (1-1820)			
Qy	1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20		
Db	1028 GGCAACCCATACGAATAAAAGTGAGAAGCTGAAAGAAAATCGCATGACTCAGACA 1087		
Qy	21 ThrGlnGluLeCysGlu 26		
Db	1088 ACGCAAGAAATATGTGAA 1105		
RESULT 9			
AX304503/c	1820 bp DNA linear PAT 30-NOV-2001		
LOCUS	AX304503		
DEFINITION	Sequence 17 from Patent WO0185947.		
ACCESSION	AX304503		
VERSION	AX304503.1 GI:17383864		
KEYWORDS			
SOURCE	Babesia microti.		
ORGANISM	Babesia microti.		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;		
AUTHORS	1 (sites)		
TITLE	Reed,S.G., Lodes,M.J., Houghton,R.L., Sleath,P.R., McNeill,P.D., Homer,M.J. and Secrist,H.		
JOURNAL	Compounds and methods for the diagnosis and treatment of Babesia microti infection		
FEATURES	Location/Qualifiers		
source	1..1820		
BASE COUNT	402 a 398 c 334 g 686 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	7e-12	Length:	1820
Score:	139.00	Matches:	26
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-794-764-195 (1-26) x AX304503 (1-1820)			
Qy	1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20		
Db	733 GGCAACCCATACGAATAAAAGTGAGAAGCTGAAAGAAAATCGCATGACTCAGACA 734		
Qy	21 ThrGlnGluLeCysGlu 26		
Db	733 ACGCAAGAAATATGTGAA 716		
RESULT 10			
AX304523	1820 bp DNA linear PAT 30-NOV-2001		
LOCUS	AX304523		
DEFINITION	Sequence 37 from Patent WO0185947.		
ACCESSION	AX304523		
VERSION	AX304523.1 GI:17383865		
KEYWORDS			
SOURCE	Babesia microti.		
ORGANISM	Babesia microti		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;		
AUTHORS	1 (sites)		
TITLE	Reed,S.G., Lodes,M.J., Houghton,R.L., Sleath,P.R., McNeill,P.D., Homer,M.J. and Secrist,H.		
JOURNAL	Compounds and methods for the diagnosis and treatment of Babesia microti infection		
FEATURES	Location/Qualifiers		
source	1..1820		
BASE COUNT	402 a 398 c 334 g 686 t		
ORIGIN			

FEATURES
source
CORIXA CORPORATION (US)
Location/Qualifiers
1..1820
/organism="Babesia microti"
/db_xref="taxon:5868"
BASE COUNT 686 a 334 c 398 g 402 t
ORIGIN

Alignment Scores:
Pred. No.: 7e-12 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-794-764-195 (1-26) x AX304523 (1-1820)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1028 GGCAAAACCAATACGAATAAAGTGAGAAGCTGAAAGAAATCGCATGATCTACTCAGACA 1087

QY 21 ThrGlnGluLeuCysGlu 26
Db 1088 ACGCAAGAAATATGTGAA 1105

RESULT 11
AX304570
LOCUS AX304570 2001 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 84 from Patent WO0185947.
ACCESSION AX304570
VERSION AX304570.1 GI:17383839
KEYWORDS
SOURCE Babesia sp.
ORGANISM Babesia sp.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
REFERENCE
AUTHORS Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., McNeill, P.D.,
Homer, M.J. and Secrist, H.
TITLE Compounds and methods for the diagnosis and treatment of Babesia
microti infection
JOURNAL Patent: WO 0185947-A 84 15-NOV-2001;
CORIXA CORPORATION (US)
FEATURES
source
1..2001
/organism="Babesia sp."
/db_xref="taxon:35084"
BASE COUNT 742 a 334 c 462 g 463 t
ORIGIN

Alignment Scores:
Pred. No.: 7.74e-12 Length: 2001
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-794-764-195 (1-26) x AX304570 (1-2001)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1207 GGCAAAACCAATACGAATAAAGTGAGAAGCTGAAAGAAATCGCATGATCTACTCAGACA 1266

QY 21 ThrGlnGluLeuCysGlu 26
Db 1267 ACGCAAGAAATATGTGAA 1284

RESULT 12
AX304629
LOCUS AX304629 2034 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 143 from Patent WO0185947.

ACCESSION AX304629
VERSION AX304629.1 GI:17383934
KEYWORDS
SOURCE Babesia sp.
ORGANISM Babesia sp.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
REFERENCE
AUTHORS Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., McNeill, P.D.,
Homer, M.J. and Secrist, H.
TITLE Compounds and methods for the diagnosis and treatment of Babesia
microti infection
JOURNAL Patent: WO 0185947-A 143 15-NOV-2001;
CORIXA CORPORATION (US)
FEATURES
source
1..2034
/organism="Babesia sp."
/db_xref="taxon:35084"
BASE COUNT 746 a 343 c 472 g 473 t
ORIGIN

Alignment Scores:
Pred. No.: 7.87e-12 Length: 2034
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-794-764-195 (1-26) x AX304629 (1-2034)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 523 GGCAAAACCAATACGAATAAAGTGAGAAGCTGAAAGAAATCGCATGATCTACTCAGACA 582

QY 21 ThrGlnGluLeuCysGlu 26
Db 583 ACGCAAGAAATATGTGAA 600

RESULT 13
AX304696
LOCUS AX304696 2079 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 210 from Patent WO0185947.
ACCESSION AX304696
VERSION AX304696.1 GI:17383965
KEYWORDS
SOURCE Babesia microti.
ORGANISM Babesia microti
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
REFERENCE
AUTHORS Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., McNeill, P.D.,
Homer, M.J. and Secrist, H.
TITLE Compounds and methods for the diagnosis and treatment of Babesia
microti infection
JOURNAL Patent: WO 0185947-A 210 15-NOV-2001;
CORIXA CORPORATION (US)
FEATURES
source
1..2079
/organism="Babesia microti"
/db_xref="taxon:5868"
BASE COUNT 782 a 354 c 422 g 521 t
ORIGIN

Alignment Scores:
Pred. No.: 8.06e-12 Length: 2079
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-794-764-195 (1-26) x AX304696 (1-2079)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
|||||
Db 1287 GCCAAACCAATACCAATAAAAGTGAGAGGCTGAAGAAAAATCGCATGATCTCAGACA 1346
Qy 21 ThrGlnGluIleCysGlu 26
|||||
Db 1347 ACGAAGAAATATGTGAA 1364
RESULT 14
AX304572 AX304572 3402 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 86 from Patent W00185947.
ACCESSION AX304572
VERSION AX304572.1 GI:17383890
KEYWORDS
SOURCE Babesia sp.
ORGANISM Babesia sp.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
REFERENCE 1 (sites)
AUTHORS Reed,S.G., Lodes,M.J., Houghton,R.L., Sleath,P.R., Mcneill,P.D.,
Homer,M.J. and Secrist,H.
TITLE Compounds and methods for the diagnosis and treatment of Babesia
microti infection
JOURNAL Patent: WO 0185947-A 86 15-NOV-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..3402
/organism="Babesia sp."
/db_xref="taxon:35084"
BASE COUNT 1184 a 615 c 712 g 891 t
ORIGIN
Alignment Scores:
Pred.No.: 1.36e-11 Length: 3402
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-794-764-195 (1-26) x AX304572 (1-3402)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
|||||
Db 2605 GCCAAACCAATACCAATAAAAGTGAGAGGCTGAAGAAAAATCGCATGATCTCAGACA 2664
Qy 21 ThrGlnGluIleCysGlu 26
|||||
Db 2665 ACGAAGAAATATGTGAA 2682
RESULT 15
AC020862/c
LOCUS AC020862 200094 bp DNA linear HTG 29-MAR-2000
DEFINITION Mus musculus clone RP23-248G14, WORKING DRAFT SEQUENCE, 52
unordered pieces.
ACCESSION AC020862
VERSION AC020862.2 GI:7340301
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 200094)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 200094)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Mar 29, 2000 this sequence version replaced gi:6686446.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----Summary Statistics
Consensus quality: 131468 bases at least Q40
Consensus quality: 161121 bases at least Q30
Consensus quality: 172522 bases at least Q20
Estimated insert size: 200094; sum-of-contigs estimation
Estimated insert size: 194000; pulse field gel estimation
Quality coverage: 3.14x in Q20 bases; pulse field gel estimation
Quality coverage: 3.05x in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 52 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1123: contig of 1123 bp in length
* gap of unknown length
* 1124 2480: contig of 1357 bp in length
* gap of unknown length
* 2481 3689: contig of 1209 bp in length
* gap of unknown length
* 3690 4967: contig of 1278 bp in length
* gap of unknown length
* 4968 5997: contig of 1030 bp in length
* gap of unknown length
* 5998 7349: contig of 1352 bp in length
* gap of unknown length
* 7350 8832: contig of 1483 bp in length
* gap of unknown length
* 8833 9879: contig of 1047 bp in length
* gap of unknown length
* 9880 11185: contig of 1306 bp in length
* gap of unknown length
* 11186 12905: contig of 1720 bp in length
* gap of unknown length
* 12906 14190: contig of 1285 bp in length
* gap of unknown length
* 14191 15635: contig of 1445 bp in length
* gap of unknown length
* 15636 16930: contig of 1295 bp in length
* gap of unknown length
* 16931 18376: contig of 1446 bp in length
* gap of unknown length
* 18377 20346: contig of 1970 bp in length
* gap of unknown length
* 20347 22028: contig of 1682 bp in length
* gap of unknown length
* 22029 23853: contig of 1825 bp in length
* gap of unknown length
* 23854 25196: contig of 1343 bp in length
* gap of unknown length
* 25197 26712: contig of 1516 bp in length
* gap of unknown length
* 26713 28473: contig of 1761 bp in length
* gap of unknown length
* 28474 29662: contig of 1189 bp in length
* gap of unknown length
* 29663 31346: contig of 1684 bp in length
* gap of unknown length
* 31347 32719: contig of 1373 bp in length
* gap of unknown length
* 32720 34057: contig of 1338 bp in length
* gap of unknown length
* 34058 36039: contig of 1982 bp in length
* gap of unknown length
* 36040 37862: contig of 1823 bp in length

*	37863	39563:	gap of 1701 bp in length
*	39564	41018:	gap of unknown length
*	41019	42986:	gap of 1455 bp in length
*	42987	44994:	gap of unknown length
*	44995	47720:	gap of 1968 bp in length
*	47721	50900:	gap of unknown length
*	50901	54324:	gap of 3180 bp in length
*	54325	58498:	gap of unknown length
*	58499	62290:	gap of 3424 bp in length
*	62291	67699:	gap of unknown length
*	67700	72719:	gap of 5409 bp in length
*	72720	78606:	gap of unknown length
*	78607	85624:	gap of 5020 bp in length
*	85625	92160:	gap of unknown length
*	92161	98561:	gap of 6536 bp in length
*	98562	105678:	gap of unknown length
*	105679	111168:	gap of 7117 bp in length
*	111169	119079:	gap of unknown length
*	119080	128003:	gap of 5490 bp in length
*	128004	134621:	gap of unknown length
*	134622	142334:	gap of 7911 bp in length
*	142335	152949:	gap of unknown length
*	152950	161984:	gap of 8924 bp in length
*	161985	171417:	gap of unknown length
*	171418	185089:	gap of 6618 bp in length
*	185090	200094:	gap of unknown length
*			gap of 9035 bp in length
*			gap of unknown length
*			gap of 9433 bp in length
*			gap of unknown length
*			gap of 10615 bp in length
*			gap of unknown length
*			gap of 13672 bp in length
*			gap of unknown length
*			gap of 15005 bp in length.

BASE COUNT	57012 a	42625 c	42956 g	57350 t	151 others
ORIGIN					

Alignment Scores:		
Pred. No.:	75.3	Length:
Score:	68.00	Matches:
Percent Similarity:	69.57%	Conservative:
Best Local Similarity:	56.53%	Mismatches:
Query Match:	48.93%	Indels:
DB:	2	Gaps:
		200094
		13
		Conservative:
		7
		Mismatches:
		0
		Indels:
		0
		Gaps:
		0

US-09-794-764-195 (1-26) x AC020862 (1-200094)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
||||| ||||| ||||| ||||| ||||| ||||| :|||
Db 47997 GGAAGACAGAATACAGAAAAAGAAAGAAAACAGAAACAGAACAGAAACACACAAGA 47938

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853079

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2002, 18:42:28 ; Search time 39 Seconds
(without alignments)
163.756 Million cell updates/sec

Title: US-09-794-764-195

Perfect score: 139

Sequence: 1 GKPNTNKSEKAKSHDTQTTOICE 26

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2_1/USPTO_spool/US09794764/runat_12102002_184218_5239/app_query.fasta_1.199
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09794764 -CGN_1_1_20 -runat_12102002_184218_5239 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NKG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	1460	4	US-08-845-258-51
2	139	100.0	1460	4	US-08-990-571-51
3	139	100.0	1820	4	US-08-845-258-17
4	139	100.0	1820	4	US-08-845-258-37
5	139	100.0	1820	4	US-08-990-571-17
6	139	100.0	1820	4	US-08-990-571-37
7	139	100.0	1820	4	US-08-723-142A-17
8	139	100.0	1820	4	US-08-723-142A-37
9	54	38.8	43676	3	US-09-356-952-12
10	48	34.5	6755	3	US-08-931-999-4
11	47	33.8	634	2	US-08-222-719-15
12	47	33.8	634	2	US-08-470-925-15

13	47	33.8	634	2	US-08-471-613-15	Sequence 15, Appl
14	47	33.8	634	5	PCT-US93-10443-15	Sequence 15, Appl
15	47	33.8	1312	2	US-08-841-349-6	Sequence 3, Appl
16	47	33.8	6960	2	US-08-841-349-3	Sequence 3, Appl
17	47	33.8	8176	2	US-08-841-349-5	Sequence 14, Appl
18	46	33.1	356	1	US-08-423-383-14	Sequence 14, Appl
19	46	33.1	356	2	US-08-437-353A-14	Sequence 14, Appl
20	46	33.1	1048	4	US-09-185-160-8	Sequence 1, Appl
21	46	33.1	1758	5	PCT-US92-01015-1	Sequence 1, Appl
22	46	33.1	2454	4	US-09-185-160-12	Sequence 12, Appl
23	46	33.1	2850	1	US-08-503-172-5	Sequence 5, Appl
24	46	33.1	2850	2	US-09-135-211-5	Sequence 5, Appl
25	46	33.1	10342	4	US-08-972-927-5	Sequence 5, Appl
26	45.5	32.7	2631	1	US-08-785-429-1	Sequence 1, Appl
27	45.5	32.7	2631	3	US-08-996-621-1	Sequence 1, Appl
28	45	32.4	278	4	US-08-905-223-199	Sequence 199, App
29	45	32.4	778	3	US-09-188-930-210	Sequence 210, App
30	45	32.4	783	3	US-09-188-930-205	Sequence 205, App
31	45	32.4	794	3	US-09-188-930-41	Sequence 41, Appl
32	45	32.4	797	3	US-09-188-930-35	Sequence 35, Appl
33	45	32.4	1230	4	US-09-172-841-52	Sequence 52, Appl
34	45	32.4	1465	4	US-09-338-671-1	Sequence 1, Appl
35	45	32.4	1926	4	US-09-590-020-1	Sequence 1, Appl
36	45	32.4	1926	4	US-09-590-020-3	Sequence 3, Appl
37	45	32.4	1926	4	US-09-590-020-5	Sequence 5, Appl
38	45	32.4	2437	2	US-08-794-216-2	Sequence 2, Appl
39	45	32.4	2496	1	US-08-073-384C-2	Sequence 2, Appl
40	45	32.4	2496	1	US-08-254-359A-2	Sequence 2, Appl
41	45	32.4	2496	1	US-08-483-043-2	Sequence 2, Appl
42	45	32.4	2496	1	US-08-481-238-2	Sequence 2, Appl
43	45	32.4	2496	2	US-08-471-056B-2	Sequence 2, Appl
44	45	32.4	2496	2	US-08-484-956-2	Sequence 2, Appl
45	45	32.4	2496	2	US-08-757-653-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-845-258-51
; Sequence 51, Application US/08845258
; Patent No. 6183976
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; AND TREATMENT OF B. MICROTI INFECTION
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,258
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206)682-6031
; INFORMATION FOR SEQ ID NO: 51:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Babesia Microti
US-08-845-258-51

Alignment Scores:
Pred. No.: 4,3e-15 Length: 1460
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-794-764-195 (1-26) x US-08-845-258-51 (1-1460)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1287 GCACAAACCAATACGAATAAAGTGAGAAGGCTGAAGAAATCCGATGATCTCAGACA 1346

Qy 21 ThrGlnGluIleCysGlu 26
Db 1347 ACGCAAGAAATATGTGAA 1364

RESULT 2
US-08-990-571-51
; Sequence 51, Application US/08990571
; Patent No. 6214971
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G. et al.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,571
; FILING DATE: 11-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Babesia Microti
US-08-990-571-51

Alignment Scores:
Pred. No.: 4,3e-15 Length: 1460
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-794-764-195 (1-26) x US-08-845-258-51 (1-1460)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1287 GCACAAACCAATACGAATAAAGTGAGAAGGCTGAAGAAATCCGATGATCTCAGACA 1346

Qy 21 ThrGlnGluIleCysGlu 26
Db 1347 ACGCAAGAAATATGTGAA 1364

RESULT 2
US-08-990-571-51
; Sequence 51, Application US/08990571
; Patent No. 6214971
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G. et al.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,571
; FILING DATE: 11-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Babesia Microti
US-08-990-571-51

Alignment Scores:
Pred. No.: 4,3e-15 Length: 1460
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-794-764-195 (1-26) x US-08-845-258-51 (1-1460)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1287 GCACAAACCAATACGAATAAAGTGAGAAGGCTGAAGAAATCCGATGATCTCAGACA 1346

Qy 21 ThrGlnGluIleCysGlu 26
Db 1347 ACGCAAGAAATATGTGAA 1364

RESULT 3
US-08-845-258-17/c
; Sequence 17, Application US/08845258
; Patent No. 6183976
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,258
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-845-258-17

Alignment Scores:
Pred. No.: 5,74e-15 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-794-764-195 (1-26) x US-08-845-258-17 (1-1820)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 793 GCACAAACCAATACGAATAAAGTGAGAAGGCTGAAGAAATCCGATGATCTCAGACA 734

Qy 21 ThrGlnGluIleCysGlu 26
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Db 733 ACGCAAGAAATATGTGAA 1105
RESULT 4
US-08-845-258-37
; Sequence 37, Application US/08845258
; Patent No. 6183976
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; AND TREATMENT OF B. MICROTI INFECTION
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,258
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-845-258-37
Alignment Scores:
Pred. No.: 5,74e-15 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-794-764-195 (1-26) x US-08-845-258-37 (1-1820)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 1028 GGCAACCCCAATACGAATAAAGTGAGAGGCTGAAGAAATCGCATGACTACTAGACA 1087
Qy 21 ThrGlnGluLeuCysGlu 26
Db 1088 ACGCAAGAAATATGTGAA 1105
RESULT 5
US-08-990-571-17/c
; Sequence 17, Application US/08990571
; Patent No. 6214971
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G. et al.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,571
; FILING DATE: 11-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-990-571-17
Alignment Scores:
Pred. No.: 5,74e-15 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-794-764-195 (1-26) x US-08-990-571-17 (1-1820)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 793 GGCAACCCCAATACGAATAAAGTGAGAGGCTGAAGAAATCGCATGACTACTAGACA 734
Qy 21 ThrGlnGluLeuCysGlu 26
Db 733 ACGCAAGAAATATGTGAA 716
RESULT 6
US-08-990-571-37
; Sequence 37, Application US/08990571
; Patent No. 6214971
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G. et al.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,571
; FILING DATE: 11-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:


```
QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1028 GGCAAAACCAATACGAATAAACTGAGAGGCTGAAAGAAATCGCATGATCTACGACA 1087

QY 21 ThrGlnGluLeuLysGlu 26
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1088 ACAGCAAGAAATATGTGAA 1105.

RESULT 9
US-09-356-952-12
; Sequence 12, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Boriack-Stodin, Ann
; APPLICANT: Margarit, S. M.
; APPLICANT: Bor-Sogii, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: 600-1-228N
; CURRENT APPLICATION NUMBER: US/09/356,952
; CURRENT FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 60/093,631
; EARLIER FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 43676
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-12

Alignment Scores:
Pred. No.: 278 Length: 43676
Score: 54.00 Matches: 9
Percent Similarity: 70.00% Conservative: 5
Best Local Similarity: 45.00% Mismatches: 6
Query Match: 38.85% Indels: 0
DB: 3 Gaps: 0

US-09-794-764-195 (1-26) x US-09-356-952-12 (1-43676)

QY 3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrGln 22
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4518 CCGAATTCCAATTCGAATATAATTCACAGAAAATCCAGGGATGACCAACCGATGAA 4577

RESULT 10
US-08-931-999-4
; Sequence 4, Application US/08931999
; Patent No. 6043219
; GENERAL INFORMATION:
; APPLICANT: Iandolo, John J.
; APPLICANT: Crupper, Scott S.
; TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,999
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/710,561
; FILING DATE: 19-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25043-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6755 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus aureus
; STRAIN: UT0007
US-08-931-999-4

Alignment Scores:
Pred. No.: 267 Length: 6755
Score: 48.00 Matches: 8
Percent Similarity: 76.47% Conservative: 5
Best Local Similarity: 47.06% Mismatches: 4
Query Match: 34.53% Indels: 0
DB: 3 Gaps: 0

US-09-794-764-195 (1-26) x US-08-931-999-4 (1-6755)

QY 3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGln 19
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2044 CCCAACGAGGAGGAAAGGCAAGAAAAAAGAGAGCCACCACACAAAG 2094

RESULT 11
US-08-222-719-15
; Sequence 15, Application US/08222719
; Patent No. 5846711
; GENERAL INFORMATION:
; APPLICANT: David D. Moore
; APPLICANT: Jae Woon Lee
; TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
; TITLE OF INVENTION: RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,719
; FILING DATE: 04-April-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,136
; FILING DATE: 30-October-1992
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/229001
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-222-719-15
Alignment Scores:
Pred. No.: 17.8 Length: 634
Score: 47.00 Matches: 9
Percent Similarity: 54.17% Conservative: 4
Best Local Similarity: 37.50% Mismatches: 11
Query Match: 33.81% Indels: 0
DB: 2 Gaps: 0
US-09-794-764-195 (1-26) x US-08-222-719-15 (1-634)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 274 GGAAGGAGGTACTGCACCATCTGAAATGCTGAACCTAAAGCTGAAGAGGCACAGAAA 333
Qy 21 ThrGlnGluLe 24
Db 334 ACTGAATCTGTA 345
RESULT 12
US-08-470-925-15
; Sequence 15, Application US/08470925
; Patent No. 5866686
; GENERAL INFORMATION:
; APPLICANT: David D. Moore
; TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
; TITLE OF INVENTION: RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,925
; FILING DATE: 06-June-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222,719
; FILING DATE: 04-April-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: 07/969,136
; FILING DATE: October 30, 1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/229003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-8906
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-470-925-15
Alignment Scores:
Pred. No.: 17.8 Length: 634
Score: 47.00 Matches: 9
Percent Similarity: 54.17% Conservative: 4
Best Local Similarity: 37.50% Mismatches: 11
Query Match: 33.81% Indels: 0
DB: 2 Gaps: 0
US-09-794-764-195 (1-26) x US-08-470-925-15 (1-634)
Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 274 GGAAGGAGGTACTGCACCATCTGAAATGCTGAACCTAAAGCTGAAGAGGCACAGAAA 333
Qy 21 ThrGlnGluLe 24
Db 334 ACTGAATCTGTA 345
RESULT 13
US-08-471-613-15
; Sequence 15, Application US/08471613
; Patent No. 5962256
; GENERAL INFORMATION:
; APPLICANT: David D. Moore
; APPLICANT: Jae Woon Lee
; TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
; TITLE OF INVENTION: RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,613
; FILING DATE: 06-June-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222,719
; FILING DATE: 04-April-1994
; CLASSIFICATION: 436
; APPLICATION NUMBER: 07/969,136
; FILING DATE: October 30, 1992
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/229001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-471-613-15
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853679

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2002, 18:42:27 : Search time 1584 Seconds
(without alignments)
221.541 Million cell updates/sec

Title: US-09-794-764-195

Perfect score: 139

Sequence: 1 GKPNNTKSEAKRSHDTQTQTEICE 26

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPfo_spool/US09794764/runat_12102002_184218_5229/app_query.fasta_1.199
-DB=EST -QFMT=fastap -SUFFIX=ist -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HFAPISE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09794764 -CGN_1_1_1144_@runat_12102002_184218_5229 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	45.3	453	12	AQ615735
2	60.5	43.5	771	10	BJ124088

ALIGNMENTS

RESULT 1	AQ615735	453 bp	DNA	linear	GSS 15-JUN-1999
LOCUS	HS_5143_A2_E06_SP6E	RPIC1-11	Human Male	BAC Library	Homo sapiens
DEFINITION	genomic clone	Plate-719	Col-12	Row-I	DNA sequence.
ACCESSION	AQ615735.1	GI:5077011			
VERSION	AQ615735				
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 453) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Kellar,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.				
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome				
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)				
MEDLINE	99380589				
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887				

Percent Similarity: 70.83%
 Best Local Similarity: 54.17%
 Query Match: 43.53%
 DB: 10

Conservative: 4
 Mismatches: 2
 Indels: 5
 Gaps: 1

US-09-794-764-195 (1-26) x BG121328 (1-1321)

Qy 4 AsnThrAsnLysSerGluLysAlaGluArgLysSerHis-----AspThr 18
 |||||
 Db 1014 AACACACACAGACAGAGACAAACACACAGACGAGGACTCACACGAGACC 1073
 |||||

Qy 19 GlnThrThrGln 22
 |||||

Db 1074 CAACACACACAG 1085
 |||||

RESULT 4

LOCUS AW698464/c
 DEFINITION g419 glandular-haired subtracted cDNA library Medicago sativa cDNA,
 mRNA sequence.

ACCESSION AW698464

VERSION AW698464.1 GI:7581050

KEYWORDS EST.

SOURCE Medicago sativa.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 390)

AUTHORS Hays, D. and Skinner, D.

TITLE Expressed sequence tags subtracted in reciprocal fashion between

JOURNAL glandular-haired and non-glandular-haired full sibs of alfalfa

COMMENT Unpublished (2000)

Contact: Hays DB

USDA, ARS, GMPRC, PSEUR; Department of Agronomy

Kansas State University

Throckmorton Hall, Manhattan, KS 66506, USA

Tel: 785 532 7116

Fax: 785 532 6167

Email: dhays@genes.alfalfa.ksu.edu

Seq primer: SP6.

Location/Qualifiers

1..390

/organism="Medicago sativa"

/cultivar="Riley X KS224"

/db_xref="taxon:3879"

/clone_lib="glandular-haired subtracted cDNA library"

/tissue_type="leaf and stem"

/note="glandular-haired versus non-glandular-haired

reciprocal cDNA subtraction with CLONTECH PCR-Select cDNA

subtraction."

BASE COUNT 107 a 101 c 74 g 108 t

ORIGIN

Alignment Scores:

Pred. No.: 79.5 Length: 390

Score: 60.00 Matches: 12

Percent Similarity: 73.91% Conservative: 5

Best Local Similarity: 52.17% Mismatches: 6

Query Match: 43.17% Indels: 0

DB: 9 Gaps: 0

US-09-794-764-195 (1-26) x AW698464 (1-390)

Qy 3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrGln 22
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Db 384 CCATGTTAAACAAAGCCCAAGCGAAACCTAGAAAGTCATCTCAGTCAAAACATATGAA 325
 |||||

Qy 23 GluIleCys 25
 |||||

Db 324 CAAATCTGT 316
 |||||

RESULT 5

LOCUS AZ015973

DEFINITION

RPci-23-290C2.TJ RPci-23 Mus musculus genomic clone RPci-23-290C2,
 DNA sequence.

ACCESSION AZ015973

VERSION AZ015973

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 477)

AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akiruet
 B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
 and Fraser, C.M.

TITLE Mouse BAC End Sequences from Library RPci-23

JOURNAL Unpublished (1999)

COMMENT Other_GSSs: RPci-23-290C2.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPci-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)

or from Resea ch Genetics (inforesgen.com). BAC end page:

http://www.tigr.org/tldb/bac.ends/mouse/bac_end_intro.html

Plate: 290 row: C column: 2

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1..477

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone_lib="RPci-23-290C2"

/lab_host="DH10B"

/sex="Female"

/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site:1:
 EcoRI; Site:2: EcoRI; Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of EcoRI and EcoRI Methyase. Size

selected DNA was cloned into the pBAC3.6 vector at the

EcoRI sites. The ligation products were transformed into

DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 176 a 108 c 79 g 113 t

ORIGIN

Alignment Scores:

Pred. No.: 136 Length: 477

Score: 59.00 Matches: 13

Percent Similarity: 62.96% Conservative: 4

Best Local Similarity: 48.15% Mismatches: 8

Query Match: 42.45% Indels: 2

DB: 12 Gaps: 1

US-09-794-764-195 (1-26) x AZ015973 (1-477)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisasp-----Thr 18
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Db 48 GGAAAAACAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 107
 |||||

Qy 19 GlnThrThrGlnIleCys 25
 |||||

Db 108 AAACCACTTTAGAAATTTGT 128
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RESULT 6

Qy 3 ProAsnThrAsnLysSerGluLysAlaGluArgLys--SerHisAspThrGlnThrThr 21

BG753600	1300 bp	linear	EST 15-MAY-2001
LOCUS	BG753600	mRNA	
DEFINITION	602733176F1 NIH_MCC_43 Homo sapiens cDNA clone IMAGE:4876482 5', mRNA sequence.		
ACCESSION	BG753600		
VERSION	BG753600.1	GI:14064253	

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
Mungali, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
, G.M.
BDGP/HMI RH Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: RH.132 row: F column: 1
High quality sequence stop: 235.
FEATURES
source
1..238
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RH13261"
/pflc="1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
BASE COUNT      81 a   47 c   61 g   48 t
ORIGIN
Alignment Scores:
Pred. No.:      117      Length:      238
Score:          57.00    Matches:     12
Percent Similarity: 58.33% Conservative:  2
Best Local Similarity: 50.00% Mismatches:    10
Query Match:      41.01% Indels:         0
DB:              10      Gaps:         0

US-09-794-764-195 (1-26) x BI608655 (1-238)
Qy  1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db  51 GCGGTCTCAAAATACAAAAAAGCGGAAAGGAATCAATTAAACAGTAGTGCTCAACAAACG 110
Qy  21 ThrGlnGlu 24
Db  111 GCCCAGGAAGTC 122

Search completed: October 12, 2002, 21:22:28
Job time : 1589 secs

TITLE
JOURNAL
COMMENT

R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
Mungali, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
, G.M.
BDGP/HMI RH Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: RH.132 row: F column: 1
High quality sequence stop: 235.
FEATURES
source
1..238
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RH13261"
/pflc="1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
BASE COUNT      81 a   47 c   61 g   48 t
ORIGIN
Alignment Scores:
Pred. No.:      117      Length:      238
Score:          57.00    Matches:     12
Percent Similarity: 58.33% Conservative:  2
Best Local Similarity: 50.00% Mismatches:    10
Query Match:      41.01% Indels:         0
DB:              10      Gaps:         0

US-09-794-764-195 (1-26) x BI608655 (1-238)
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Qy  21 ThrGlnGlu 24
Db  111 GCCCAGGAAGTC 122

Search completed: October 12, 2002, 21:22:28
Job time : 1589 secs

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